SEQUENCE LISTING

<110> Hua, Shao-bing
Pauling, Michelle H.
Zhu, Li

<120> HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS

<130> 25636-718

<160> 54

<170> PatentIn version 3.1

<210> 1
<211> 352
<212> PRT
<213> Homo sapiens

<400> 1

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
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Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

<210> 2
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<212> PRT
<213> Homo sapiens

<400> 2

Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp
1 5 10 15

Gln

<210> 3
<211> 29
<212> PRT
<213> Homo sapiens

<400> 3

Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln
1 5 10 15

Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His Cys
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<210> 4
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> G4S Linker

<400> 4

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Gly Gly Gly Ser
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<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA of G4S Linker

<400> 5
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<213> Artificial Sequence

<220>
<223> 5' Homologous Sequence

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<210> 7
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Homologous Sequence

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<211> 36
<212> PRT
<213> Homo sapiens

<400> 8

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30

Leu Pro Pro Leu
35

<210> 9
<211> 32
<212> PRT
<213> Homo sapiens

<400> 9

Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe
1 5 10 15

Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile
20 25 30

<210> 10
<211> 30
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<213> Artificial Sequence

<220>
<223> Primer

<400> 10

ggagaattcg attatcaagt gtcaagtcca
30

<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
cgcggatcct tagagcggag gcaggaggcg g
31

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
ggagaattca ccagatctca aaaagaagg
29

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
cgcggatcct tatatcttta atgtctggaa att
33

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
caggaattct ttggcctgaa t
21

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
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31

<210> 16
<211> 759
<212> DNA
<213> Artificial Sequence

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acctgcacct tgtctgggtt ctcactcagc actagtggag tgagtgtggg ctggatccgt
120

cagcccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc
180

tacagcccat ctctgaaaag caggctcacc atcaccaagg acacccccaa aaaccaggtg
240

gtccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat
300

acaatggtca ccgtctcttc aggcggtggt ggatcaggcg gcggaggatc tggcggaggt
420

ggcagcggtg gtggaggcag ttcctatgag ctgatgcagc taccctcagt gtccgtgtcc
480

ccaggacaga cagccagcat cacctgctct ggagataatt tgggggataa atatgcctgc
540

tggtatcaac agaagccagg ccggtcccct gtgctggtca tttatggaga taacaagcgg
600

ccctcaggga tccctgagcg attctctggc tccaactctg ggaacacagc cactctgacc
660

atcagcggga cccaggctat ggatgaggct gactattact gtcaggcgtg ggacaccagc
720

actgctgtct tcggaactgg gaccaagctc accgtccta
759

<210> 17
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.186.35

<400> 17

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser
50 55 60

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Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val
65                  70                  75                  80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser
                85                  90                  95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp
            100                 105                 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

Gly Gly Ser Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser
145                 150                 155                 160

Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp
                165                 170                 175

Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu
            180                 185                 190

Val Ile Tyr Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
        195                 200                 205

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
    210                 215                 220

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser
225                 230                 235                 240

Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
                245                 250
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<210> 18
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.150.11

<400> 18
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acttgcactg tctctggtgg ctccatcggt catgactact ggagctggat acggcagccc
120

ccaggggagg gactggagtg gattggtttc atcttcttcg atgggagcac caactacaac
180

ccctccctca acggtcgagt caccatctca ctcgacacgt cgaagaatca gctctccctg
240

aaggctgacct ctgtgaccgc tgcggacacg gccgtgtatt tctgtgcgag actaaagggg
300

gcgtggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa
360

gggaccacgg tcaccgtccc ctcaggcggt ggtggatcag gcggcggagg atctggcgga
420

ggtggcagcg gtggtggagg cagtaatttt atgctgactc agccccctc agcgtctggg
480

acccccgggc agagggtcag catctcttgt tctgggagca gctccgacat cggaagtaat
540

actgtaaact ggtaccagca actcccagga acggccccca aactcctcat ctatagtaat
600

aatcagcggc cctcaggggt ccctgaccga ttctctggct tcaagtctgg cacctcagcc
660

tccctggtca tcagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg
720

gatgagagcc tgaatggtgt ggtgttcggc ggaggaccaa gg
762

<210> 19
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.11

<400> 19

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser
100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Pro Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly

145 150 155 160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp
165 170 175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
180 185 190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro
195 200 205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile
210 215 220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp
225 230 235 240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Pro Arg
245 250

<210> 20
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.150.12

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acctgcgctg tctctggtgc gtcgtttagt ggttattatt ggagctggat ccgccagccc
120

ccagggaagg ggctggagtg gattggggag atcaatcatc gtggaagcac tacctacaac
180

ccgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt
240

aaactgacct ctatgaccgc cgcggacacg gccgtgtatt actgtgcgag gacagtggct
300

ggtactagtg actactgggg ccagggaacc ctggtcaccg tttcctcagg gagtgcatcc
360

gccccaacgg gcggtggtgg atcaggcggc ggaggatctg gcggaggtgg cagcggtggt
420

ggaggcagta aaacgacact cacgcagtct ccagcattca tgtcagcgac tccaggagac
480

aaagtcagca tctcctgcaa agccagccga gacgttgatg atgatgtgaa ctggtaccaa
540

cagagaccag gagaagctcc tattttcatt attgaagatg ctactactct cgttcctgga
600

atctcacctc gattcagtgg cagcgggtat ggaaccgatt ttaccctcac aattaataac
660

atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc
720

ttcggcggag ggaccaaggt ggagatcaaa
750

<210> 21
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.12

<400> 21

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu
65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Gly Ser Ala Ser Ala Pro Thr Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys
130 135 140

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp
145 150 155 160

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val
165 170 175

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu
180 185 190

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser
195 200 205

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu
210 215 220

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 22
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.150.24

<400> 22
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acctgcacct tctctgggtt ctcactcaga actactggag agggtgtggg ctgggtccgt
120

cagcccccag gaaaggccct ggaatggctt gcactcattt attgggatga tgataagcgc
180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaagcaggtg
240

gtccttacaa tgaccaacgt ggacccagcg gacacagcca cctattactg tacacacgag
300

caatactatt atgatactag tggtcagcca tactactttg acttctgggg ccagggcacc
360

ctggtcaccg tctcctcagg cggtggtgga tcaggcggcg gaggatctgg cggaggtggc
420

agcggtggtg gaggcagtaa catccaggtg acccagtctc catcctccct gtctgcatct
480

gtaggagaca gagtcaccat gacttgccgg gcgagtcagg acattaggaa gaatttaaat
540

tggtatcagc aaaaaccagg gaaagcccct aaggtcctga tctacgatgc atccgatttg
600

gaaacaggga tcccatcaag gttcagtgga agtggatctg ggacagattt tatcctcacc
660

atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta
720

ccgctcactt tcggcggagg gaccaaagtg gatatcaaa
759

<210> 23
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.24

<400> 23

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145 150 155 160

Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg
165 170 175

Lys Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val
180 185 190

Leu Ile Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe
195 200 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu
210 215 220

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu
225 230 235 240

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
245 250

<210> 24
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.186.35 Variant

<400> 24
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acctgcacct tgtctgggtt ctcactcagc actagtggag tgagtgtggg ctggatccgt
120

cagcccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc
180

tacagcccat ctctgaaaag caggctcacc atcaccaagg acacccccaa aaaccaggtg
240

gtccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat
300

atgccccccc atgatagtgg cccgcaatct tttgatgctt ctgatgtctg gggcccaggg
360

acaatggtca ccgtctcttc aggcggtggt ggatcaggcg gcggaggatc tggcggaggt
420

ggcagcggtg gtggaggcag ttcctatgag ctgatgcagc taccctcagt gtccgtgtcc
480

ccaggacaga cagccagcat cacctgctct ggagataatt tgggggataa atatgcctgc
540

tggtatcaac agaagccagg ccggtcccct gtgctggtca tttatggaga taacaagcgg
600

ccctcaggga tccctgagcg attctctggc tccaactctg ggaacacagc cactctgacc
660

atcagcggga cccaggctat ggatgaggct gactattact gtcaggcgtg ggacaccagc
720

actgctgtct tcggaactgg gaccaagctc accgtccta
759

<210> 25
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.186.35 Variant

<400> 25

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val
65 70 75 80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser
85 90 95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp
100 105 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser
145 150 155 160

Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp
165 170 175

Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu
180 185 190

Val Ile Tyr Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
195 200 205

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
210 215 220

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser
225 230 235 240

Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
245 250

<210> 26
<211> 774
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.150.11 Variant

<400> 26
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acttgcactg tctctggtgg ctccatcggt catgactact ggagctggat acggcagccc 120

ccaggggagg gactggagtg gattggtttc atcttcttcg atgggagcac caactacaac 180

ccctccctca acggtcgagt caccatctca ctcgacacgt cgaagaatca gctctccctg 240

aggctgacct ctgtgaccgc tgcggacacg gccgtgtatt tctgtgcgag actaaagggg 300

gcgtggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa 360

gggaccacgg tcaccgtctc ctcaggcggt ggtggatcag gcggcggagg atctggcgga 420

ggtggcagcg gtggtggagg cagtaatttt atgctgactc agccccctc agcgtctggg 480

acccccgggc agagggtcag catctcttgt tctgggagca gctccgacat cggaagtaat 540

actgtaaact ggtaccagca actcccagga acggccccca aactcctcat ctatagtaat
600

aatcagcggc cctcaggggt ccctgaccga ttctctggct tcaagtctgg cacctcagcc
660

tccctggtca tcagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg
720

gatgagagcc tgaatggtgt ggtgttcggc ggaggaacca aggtgaccgt ccta
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<210> 27
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.11

<400> 27

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser

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                100                 105                 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly
145                 150                 155                 160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp
                165                 170                 175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
            180                 185                 190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro
        195                 200                 205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile
    210                 215                 220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp
225                 230                 235                 240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Val Thr
                245                 250                 255

Val Leu
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<210> 28
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.150.12 Variant

<400> 28
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acctgcgctg tctctggtgc gtcgtttagt ggttattatt ggagctggat ccgccagccc
120

ccagggaagg ggctggagtg gattggggag atcaatcatc gtggaagcac tacctacaac
180

ccgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt
240

aaactgacct ctatgaccgc cgcggacacg gccgtgtatt actgtgcgag gacagtggct
300

ggtactagtg actactgggg ccagggaacc ctggtcaccg tttcctcagg gagtgcatcc
360

gccccaacgg gcggtggtgg atcaggcggc ggaggatctg gcggaggtgg cagcggtggt
420

ggaggcagtg aaacgacact cacgcagtct ccagcattca tgtcagcgac tccaggagac
480

aaagtcagca tctcctgcaa agccagccga gacgttgatg atgatgtgaa ctggtaccaa
540

cagagaccag gagaagctcc tattttcatt attgaagatg ctactactct cgttcctgga
600

atctcacctc gattcagtgg cagcgggtat ggaaccgatt ttaccctcac aattaataac
660

atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc
720

ttcggcggag ggaccaaggt ggagatcaaa
750

<210> 29
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.12 Variant

<400> 29

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu
65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Gly Ser Ala Ser Ala Pro Thr Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp
145 150 155 160

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val
165 170 175

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu
180 185 190

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser
195 200 205

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu
210 215 220

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 30
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.150.24 Variant

<400> 30
caggtcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg
60

acctgcacct tctctgggtt ctcactcaga actactggag agggtgtggg ctgggtccgt
120

cagccccag gaaaggccct ggaatggctt gcactcattt attgggatga tgataagcgc
180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaagcaggtg
240

gtccttacaa tgaccaacgt ggacccagcg gacacagcca cctattactg tacacacgag
300

caatactatt atgatactag tggtcagcca tactactttg acttctgggg ccagggcacc
360

ctggtcaccg tctcctcagg cggtggtgga tcaggcggcg gaggatctgg cggaggtggc
420

agcggtggtg gaggcagtaa catccaggtg acccagtctc catcctccct gtctgcatct
480

gtaggagaca gagtcaccat gacttgccgg gcgagtcagg acattaggaa gaatttaaat
540

tggtatcagc aaaaaccagg gaaagcccct aaggtcctga tctacgatgc atccgatttg
600

gaaacaggga tcccatcaag gttcagtgga agtggatctg ggacagattt tatcctcacc
660

atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta
720

ccgctcactt tcggcggagg gaccaaagtg gatatcaaa
759

<210> 31
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.24 Variant

<400> 31

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

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Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr
            100                 105                 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145                 150                 155                 160

Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg
                165                 170                 175

Lys Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val
            180                 185                 190

Leu Ile Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe
        195                 200                 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu
    210                 215                 220

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu
225                 230                 235                 240

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
                245                 250
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<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR2

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X = Asparagine or Threonine

<400> 32

Gly Ser Thr Xaa Tyr Asn Pro Ser Leu
1 5

<210> 33
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR2

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> X3 = Asparagine or Threonine
X4 = Threonine or Aspartic acid

<400> 33

Asp Ala Xaa Xaa Leu
1 5

<210> 34
<211> 127
<212> PRT
<213> Homo sapiens

<400> 34

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val
65 70 75 80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser
85 90 95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp
100 105 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 35
<211> 106
<212> PRT
<213> Homo sapiens

<400> 35

Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp Lys Tyr Ala
20 25 30

Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu Val Ile Tyr
35 40 45

Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser Thr Ala Val
85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
100 105

<210> 36
<211> 126
<212> PRT
<213> Homo sapiens

<400> 36

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala

85 90 95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser
100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
115 120 125

<210> 37
<211> 104
<212> PRT
<213> Homo sapiens

<400> 37

Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Glu Ser Leu
85 90 95

Asn Gly Val Val Phe Gly Gly Gly
100

<210> 38
<211> 116

<212> PRT
<213> Homo sapiens

<400> 38

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu
65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 39
<211> 106
<212> PRT
<213> Homo sapiens

<400> 39

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp
1 5 10 15

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val
20 25 30

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu
35 40 45

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser
50 55 60

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu
65 70 75 80

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 40
<211> 126
<212> PRT
<213> Homo sapiens

<400> 40

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val

65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 41
<211> 107
<212> PRT
<213> Homo sapiens

<400> 41

Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg Lys Asn
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 42
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker Sequence

<400> 42

Gly Gly Gly Gly Ser
1 5

<210> 43
<211> 21
<212> PRT
<213> Homo sapiens

<400> 43

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser
1 5 10 15

Asp Gly Met Asp Val
20

<210> 44
<211> 9
<212> PRT
<213> Homo sapiens

<400> 44

Arg Thr Val Ala Gly Thr Ser Asp Tyr
1 5

<210> 45
<211> 17
<212> PRT
<213> Homo sapiens

<400> 45

His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr Phe Asp
1 5 10 15

Phe

<210> 46
<211> 11
<212> PRT
<213> Homo sapiens

<400> 46

Ala Ala Trp Asp Glu Ser Leu Asn Gly Val Val
1 5 10

<210> 47
<211> 9
<212> PRT
<213> Homo sapiens

<400> 47

Leu Gln His Asp Asn Phe Pro Leu Thr
1 5

<210> 48
<211> 9
<212> PRT
<213> Homo sapiens

<400> 48

Gln Gln Ser Asp Tyr Leu Pro Leu Thr
1 5

<210> 49
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 49
ggagaattcg attatcaagt gtcaagtcca
30

<210> 50
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 50
cgcggatcct tagagcggag gcaggaggcg g
31

<210> 51
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 51
ggagaattca ccagatctca aaaagaagg
29

<210> 52
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 52
cgcggatcct tatatcttta atgtctggaa att
33

<210> 53
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 53
caggaattct ttggcctgaa t
21

<210> 54
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 54
cgcggatcct cagcagtgcg tcatcccaag a
31